

E. Lator-Wesley

# 11  
9/23/02

RAW SEQUENCE LISTING DATE: 09/23/2002  
 PATENT APPLICATION: US/09/639,273 TIME: 12:47:34

Input Set : N:\Crf3\RULE60\09639273.raw  
 Output Set: N:\CRF4\09232002\I639273.raw

-----SEQUENCE LISTING-----

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Innes, Michael  
 6 Creasey, Abla  
 8 (ii) TITLE OF INVENTION: Production of Tissue Factor Pathway  
 9 Inhibitor

11 (iii) NUMBER OF SEQUENCES: 7

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Chiron Corporation  
 15 (B) STREET: 4560 Horton St.  
 16 (C) CITY: Emeryville  
 17 (D) STATE: CA  
 18 (E) COUNTRY: USA  
 19 (F) ZIP: 94608

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk  
 23 (B) COMPUTER: IBM PC compatible  
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/639,273  
 C--> 29 (B) FILING DATE: 15-Aug-2000

30 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/286,530  
 35 (B) FILING DATE: 05-AUG-1994

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Savereide, Paul B.  
 39 (B) REGISTRATION NUMBER: 36,914  
 40 (C) REFERENCE/DOCKET NUMBER: 0991.001

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 510-601-2585  
 44 (B) TELEFAX: 510-655-3542

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1065 base pairs  
 51 (B) TYPE: nucleic acid  
 52 (C) STRANDEDNESS: double  
 53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: other nucleic acid

57 (iii) HYPOTHETICAL: NO

59 (iv) ANTI-SENSE: NO

62 (ix) FEATURE:

ENTERED

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63 (A) NAME/KEY: CDS  
64 (B) LOCATION: 1..1056  
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
69 ATG CAG ATC TTC GTC AAG ACT TTG ACC GGT AAA ACC ATA ACA TTG GAA 48  
70 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
71 1 5 10 15  
73 GTT GAA TCT TCC GAT ACC ATC GAC AAC GTT AAG TCG AAA ATT CAA GAC 96  
74 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp  
75 20 25 30  
77 AAG GAA GGT ATC CCT CCA GAT CAA CAA AGA TTG ATC TTT GCC GGT AAG 144  
78 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
79 35 40 45  
81 CAG CTA GAA GAC GGT AGA ACG CTG TCT GAT TAC AAC ATT CAG AAG GAG 192  
82 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
83 50 55 60  
85 TCC ACC TTA CAT CTT GTG CTA AGG CTC CGC GGT GAT TCT GAG GAA 240  
86 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Asp Ser Glu Glu  
87 65 70 75 80  
89 GAT GAA GAA CAC ACA ATT ATC ACA GAT ACG GAG TTG CCA CCA CTG AAA 288  
90 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys  
91 85 90 95  
93 CTT ATG CAT TCA TTT TGT GCA TTC AAG GCG GAT GAT GGC CCA TGT AAA 336  
94 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys  
95 100 105 110  
97 GCA ATC ATG AAA AGA TTT TTC TTC AAT ATT TTC ACT CGA CAG TGC GAA 384  
98 Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu  
99 115 120 125  
101 GAA TTT ATA TAT GGG GGA TGT GAA GGA AAT CAG AAT CGA TTT GAA AGT 432  
102 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser  
103 130 135 140  
105 CTG GAA GAG TGC AAA AAA ATG TGT ACA AGA GAT AAT GCA AAC AGG ATT 480  
106 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile  
107 145 150 155 160  
109 ATA AAG ACA ACA TTG CAA CAA GAA AAG CCA GAT TTC TGC TTT TTG GAA 528  
110 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu  
111 165 170 175  
113 GAA GAT CCT GGA ATA TGT CGA GGT TAT ATT ACC AGG TAT TTT TAT AAC 576  
114 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn  
115 180 185 190  
117 AAT CAG ACA AAA CAG TGT GAA CGT TTC AAG TAT GGT GGA TGC CTG GGC 624  
118 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly  
119 195 200 205  
121 AAT ATG AAC AAT TTT GAG ACA CTG GAA GAA TGC AAG AAC ATT TGT GAA 672  
122 Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu  
123 210 215 220  
125 GAT GGT CCG AAT GGT TTC CAG GTG GAT AAT TAT GGA ACC CAG CTC AAT 720  
126 Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn  
127 225 230 235 240  
129 GCT GTG AAT AAC TCC CTG ACT CCG CAA TCA ACC AAG GTT CCC AGC CTT 768

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130 Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu  
 131 245 250 255  
 133 TTT GAA TTT CAC GGT CCC TCA TGG TGT CTC ACT CCA GCA GAC AGA GGA 816  
 134 Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly  
 135 260 265 270  
 137 TTG TGT CGT GCC AAT GAG AAC AGA TTC TAC TAC AAT TCA GTC ATT GGG 864  
 138 Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly  
 139 275 280 285  
 141 AAA TGC CGC CCA TTT AAG TAC AGT GGA TGT GGG GGA AAT GAA AAC AAT 912  
 142 Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Asn Glu Asn Asn  
 143 290 295 300  
 145 TTT ACT TCC AAA CAA GAA TGT CTG AGG GCA TGT AAA AAA GGT TTC ATC 960  
 146 Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile  
 147 305 310 315 320  
 149 CAA AGA ATA TCA AAA GGA GGC CTA ATT AAA ACC AAA AGA AAA AGA AAG 1008  
 150 Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys  
 151 325 330 335  
 153 AAG CAG AGA GTG AAA ATA GCA TAT GAA GAA ATT TTT GTT AAA AAT ATG 1056  
 154 Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met  
 155 340 345 350  
 157 TGAGTCGAC 1065  
 160 (2) INFORMATION FOR SEQ ID NO: 2:  
 162 (i) SEQUENCE CHARACTERISTICS:  
 163 (A) LENGTH: 352 amino acids  
 164 (B) TYPE: amino acid  
 165 (D) TOPOLOGY: linear  
 167 (ii) MOLECULE TYPE: protein  
 169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 171 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
 172 1 5 10 15  
 174 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp  
 175 20 25 30  
 177 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 178 35 40 45  
 180 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 181 50 55 60  
 183 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Asp Ser Glu Glu  
 184 65 70 75 80  
 186 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys  
 187 85 90 95  
 189 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys  
 190 100 105 110  
 192 Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu  
 193 115 120 125  
 195 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser  
 196 130 135 140  
 198 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile  
 199 145 150 155 160  
 201 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu

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202 165 170 175  
204 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn  
205 180 185 190  
207 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly  
208 195 200 205  
210 Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu  
211 210 215 220  
213 Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn  
214 225 230 235 240  
216 Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu  
217 245 250 255  
219 Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly  
220 260 265 270  
222 Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly  
223 275 280 285  
225 Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn  
226 290 295 300  
228 Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile  
229 305 310 315 320  
231 Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys  
232 325 330 335  
234 Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met  
235 340 345 350

238 (2) INFORMATION FOR SEQ ID NO: 3:

240 (i) SEQUENCE CHARACTERISTICS:  
241 (A) LENGTH: 276 amino acids  
242 (B) TYPE: amino acid  
243 (C) STRANDEDNESS: single  
244 (D) TOPOLOGY: linear

246 (ii) MOLECULE TYPE: peptide

251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

253 Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu  
254 1 5 10 15  
256 Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp  
257 20 25 30  
259 Gly Pro Cys Arg Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr  
260 35 40 45  
262 Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn  
263 50 55 60  
265 Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn  
266 65 70 75 80  
268 Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe  
269 85 90 95  
271 Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg  
272 100 105 110  
274 Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly  
275 115 120 125  
277 Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys  
278 130 135 140

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280 Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly  
281 145 150 155 160  
283 Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys  
284 165 170 175  
286 Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro  
287 180 185 190  
289 Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn  
290 195 200 205  
292 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly  
293 210 215 220  
295 Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys  
296 225 230 235 240  
298 Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys  
299 245 250 255  
301 Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe  
302 260 265 270  
304 Val Lys Asn Met  
305 275  
307 (2) INFORMATION FOR SEQ ID NO: 4:  
309 (i) SEQUENCE CHARACTERISTICS:  
310 (A) LENGTH: 9 base pairs  
311 (B) TYPE: nucleic acid  
312 (C) STRANDEDNESS: single  
313 (D) TOPOLOGY: linear  
315 (ii) MOLECULE TYPE: other nucleic acid  
316 (A) DESCRIPTION: /desc = "primer"  
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
323 CCGCGGGGC 9

325 (2) INFORMATION FOR SEQ ID NO: 5:  
327 (i) SEQUENCE CHARACTERISTICS:  
328 (A) LENGTH: 23 base pairs  
329 (B) TYPE: nucleic acid  
330 (C) STRANDEDNESS: single  
331 (D) TOPOLOGY: linear  
333 (ii) MOLECULE TYPE: other nucleic acid  
334 (A) DESCRIPTION: /desc = "primer"  
339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
341 GCTCCGCGGT GGCGATTCTG AGG 23  
343 (2) INFORMATION FOR SEQ ID NO: 6:  
345 (i) SEQUENCE CHARACTERISTICS:  
346 (A) LENGTH: 24 base pairs  
347 (B) TYPE: nucleic acid  
348 (C) STRANDEDNESS: single  
349 (D) TOPOLOGY: linear  
351 (ii) MOLECULE TYPE: other nucleic acid  
352 (A) DESCRIPTION: /desc = "primer"  
357 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
359 TCTGTCGACT CACATATTAAAC 24  
361 (2) INFORMATION FOR SEQ ID NO: 7:

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/23/2002  
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### Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 160  
Seq#:2; Line(s) 238  
Seq#:3; Line(s) 307  
Seq#:4; Line(s) 325  
Seq#:5; Line(s) 343  
Seq#:6; Line(s) 361

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09639273.raw  
Output Set: N:\CRF4\09232002\I639273.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]